

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 15:52:19 ; Search time 170.72 Seconds
(without alignments)
27.443 Million cell updates/sec

Title: US-09-331-631A-1_COPY_117_185

Perfect score: 384
Sequence: 1 NR0RDPQOQYEQCCOKHCORR.....EEQOREDEKYEERMKERDN 69

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 195891 seqs, 67900655 residues

Total number of hits satisfying chosen parameters: 195891

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: PIR66:*
2: PIR1:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	172	44.8	566	2 S22477	vicillin precursor
2	152.5	39.7	588	1 FMCNAB	alpha-globulin B p
3	147	38.3	509	2 S08059	alpha-globulin typ
4	130.5	34.0	605	2 S06398	alpha-globulin typ
5	116.5	30.3	1038	2 T02634	rep protein homolo
6	114	29.7	810	2 T44430	protein PV100 (imp
7	105	27.3	613	2 S27770	hypothetical prote
8	105	27.3	1737	2 A59235	unconventional myo
9	104.5	27.2	385	2 T19201	hypothetical prote
10	104	27.1	1390	2 T14004	hypothetical prote
11	103.5	27.0	1898	1 A45973	trichoglycin - hum
12	102	26.6	1407	1 S28589	trichoglycin - hum
13	101	26.3	233	2 T17218	hypothetical prote
14	101	26.3	1027	2 T46481	hypothetical prote
15	101	26.3	1233	2 T30989	hypothetical prote
16	98	25.5	648	1 J01150	serine/threonine p
17	97.5	25.4	839	2 I50590	protein kinase (EC
18	97.5	25.4	877	2 I50591	class II INCENP pr
19	95	24.7	385	2 T20410	hypothetical prote
20	95	24.7	524	2 T01730	62k sucrose-bindin
21	95	24.7	781	2 T02272	hypothetical prote
22	95	24.7	849	2 S61962	probable membrane
23	95	24.7	1023	2 S12519	glutathion - fruit
24	95	24.7	1085	2 S62516	glutathion - fruit
25	94	24.5	285	1 A46207	hypothetical colle
26	94	24.5	678	2 A54514	involucrin - dog
27	93	24.2	529	2 A71899	glutamic acid-rich
28	92.5	24.1	538	2 S29521	hypothetical prote
29	92	24.0	338	2 S04321	casein kinase I ho
					legumin B (clone p

30	92	24.0	429	2 S29565	apolipoprotein A-I
31	92	24.0	523	2 T24961	hypothetical prote
32	92	24.0	566	2 T06453	probable legumin B
33	92	24.0	905	1 RGNYS5	regulatory protein
34	92	24.0	1403	2 S24548	homeotic protein p
35	91.5	23.8	406	2 T24492	hypothetical prote
36	91.5	23.8	550	2 A46419	trophoblast-endoth
37	91.5	23.8	695	2 I54325	gene xzf protein -
38	91	23.7	139	2 A26892	Mopa box protein -
39	91	23.7	483	2 T06459	62k sucrose-bindin
40	91	23.7	1344	2 T42637	hypothetical prote
41	90.5	23.6	758	2 S54522	hypothetical prote
42	90.5	23.6	1263	2 T15496	hypothetical prote
43	90	23.4	1549	1 A40691	trichoglycin - she
44	90	23.4	1905	2 T18267	multidrug resistan
45	89.5	23.3	393	2 J06179	dorsal switch prot

ALIGNMENTS

RESULT 1
S22477
vicillin precursor - cacao
C:Species: Theobroma cacao (cacao)
C:Date: 30-Sep-1993 #sequence-revision 30-Sep-1993 #text-change 17-Mar-1999
C:Accession: S22477; S22478; S18105; S22050
R:McHenry, L., Fritz, P.J., 1173-1176, 1992
Plant Mol. Biol. 18, 1173-1176, 1992
A:Title: Comparison of the structure and nucleotide sequence of vicillin genes of coco
A:Reference number: S22477; UID:92288309
A:Accession: S22477
A:Molecule type: DNA
A:Residues: 1-566 <MCU>
A:Cross-references: EMBL:X62625
A:Accession: S22478
A:Molecule type: mRNA
A:Residues: 1-452 <MC2>
A:Cross-references: EMBL:X62626
C:Genetics:
A:introns: 211/1; 269/3; 296/3; 391/3; 502/1
C:Superfamily: glycinin
C:Keywords: seed; storage protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-566/Product: vicillin #status predicted <MAT>

Query Match 44.8%; Score 172; DB 2; Length 566;
Best Local Similarity 31.4%; Pred. No. 2.6e-07;
Matches 32; Conservative 20; Mismatches 14; Indels 36; Gaps 2;
OY 3 ORPQOQYEQCCOKHCORRTERPRHMTCCORCRRREKRRKQ-----46
DB 35 ERDPQOQYEQCCOKHCORRTERPRHMTCCORCRRREKRRKQ-----46
OY 47 -----KRYEQOREDEKYEERMKERDN 68
DB 95 QQQGQOREQOQCCOKHCORRTERPRHMTCCORCRRREKRRKQ-----136

RESULT 2
FMCNAB
alpha-globulin B precursor (clone C72) - upland cotton
A:Alternate names: seed storage protein; vicillin precursor
C:Species: Gossypium hirsutum (upland cotton)
C:Date: 30-Sep-1991 #sequence-revision 30-Sep-1991 #text-change 16-Jul-1999
C:Accession: A30838; S06911
R:Chlan, C.A.; Pyle, J.B.; Legocki, A.B.; Dure III, L.
Plant Mol. Biol. 7, 475-489, 1986
A:Title: Developmental biochemistry of cottonseed embryogenesis and germination XVIII
A:Reference number: A30838
A:Accession: A30838
A:Molecule type: mRNA

[illegible]

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Query Match      27.3%; Score 105; DB 2; Length 1737;  
Best Local Similarity   36.28; Pred. No. 0.19;  
Matches    25; Conservative    20; Mismatches    4; Gaps    2;
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OY 1 NRNRPDQDQVBOCCKHOCRRRELEPRHMOTCCOORCEERYEKE-KKCOCKRYEEQQREDEEK 59
|:::~::~|| ||| | : :|| ||||::::| |::|::||

[illegible]

Query Match	27.1%	Score 104;	DB 2;	Length 190;
Best Local Similarity	23.9%	Pred.	No. 0.19;	
Matches	16;	Conservative	30;	Mismatches 21; Indels 0
QY	2	RQRDPQQGYEBCGKHCQRRRTEPRHMOTCCQCCEKRYEKERKKOQKYRYEQREDEKEYE	61	
	:	: :: :: :	:	:
Db	91	Q000P0000S000000H00000P0000P000000P000000P000000000000000P000	150	
QY	62	ERMKEED	68	
Db	151	Q00000D	157	

